O-CD2a Antibody and Uses - Sequence List(P:\OP\PATAP650)

#### SEQUENCE LISTING

- (1) GENERAL INFORMATION:
  - (i) APPLICANT: Bazin, Hervé

Latinne, Dominique

(ii) TITLE OF INVENTION: LO-CD2a Antibody and Uses

Thereof for Inhibiting T-

Cell Activation and

Proliferation

- (iii) NUMBER OF SEQUENCES: 96
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi, Stewart & Olstein
  - (B) STREET: 6 Becker Farm Road
  - (C) CITY: Roseland
  - (D) STATE: New Jersey
  - (E) COUNTRY: U.S.A.
  - (F) ZIP: 07068
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: 3.5 inch diskette
  - (B) COMPUTER: IBM PS/2
  - (C) OPERATING SYSTEM: MS-DOS
  - (D) SOFTWARE: WordPerfect 5.1
- (vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: 08/472,281
- (B) FILING DATE: 07-JUN-1995
- (C) CLASSIFICATION:

### (vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: 08/407,009
- (B) FILING DATE: 29-MAR-1995
- (A) APPLICATION NUMBER: 08/119,032
- (B) FILING DATE: 09-SEP-1993
- (A) APPLICATION NUMBER: 08/027,008
- (B) FILING DATE: 05-MAR-1993

## (viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Olstein, Elliot M.
- (B) REGISTRATION NUMBER: 24,025
- (C) REFERENCE/DOCKET NUMBER: 61750-142

# (ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 201-994-1700
- (B) TELEFAX: 201-994-1744

# (2) INFORMATION FOR SEQ ID NO: 1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 32 bases
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single

(ii)	MOLECULE TYPE: oligonucleotide	
(ix)	FEATURE:	
	(A) NAME/KEY: PCR primer	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 1:	
AACCCGGGGA CATTCAC	GCTG ACCCAGTCTC AA	32
(2)	INFORMATION FOR SEQ ID NO: 2:	
(i)	SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 29 bases	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: oligonucleotide	
(ix)	FEATURE:	
	(A) NAME/KEY: PCR primer	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 2:	
CAGTCGACTA CAGTTGG	TGC AGCATCAGC	29
(2)	INFORMATION FOR SEQ ID NO: 3:	
(i)	SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 31 bases	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	

TOPOLOGY: linear

(D)

(D) TOPOLOGY: linear (ii) MOLECULE TYPE: oligonucleotide (ix) FEATURE: (A) NAME/KEY: PCR primer (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3: AACCCGGGGA GGTCCAGCTG CAGCAGTCTG G 31 (2) INFORMATION FOR SEQ ID NO: 4: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 27 bases (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: oligonucleotide (ix) FEATURE: (A) NAME/KEY: PCR primer (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4: AAGTCGACCC AGTGGATAGA CCGATGG 27 (2) INFORMATION FOR SEQ ID NO: 5: (i) SEQUENCE CHARACTERISTICS:

· i'

(A) LENGTH: 22 bases

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

	(D) TOPOLOGY:	linear	
(ii)	MOLECULE TYPE:	oligonucleotide	
(ix)	FEATURE:		
	(A) NAME/KEY:	PCR primer	
(xi)	SEQUENCE DESCRI	PTION: SEQ ID NO: 5:	
CCGCAAGCTT CATGGGA	TGG AG		22
(2)	INFORMATION FOR	SEQ ID NO: 6:	
(i)	SEQUENCE CHARACT	TERISTICS:	
	(A) LENGTH: 27	bases	
	(B) TYPE: nucl	leic acid	
	(C) STRANDEDNES	SS: single	
	(D) TOPOLOGY:	linear	
(ii)	MOLECULE TYPE:	oligonucleotide	
(ix)	FEATURE:		
	(A) NAME/KEY:	PCR primer	
(xi)	SEQUENCE DESCRIE	PTION: SEQ ID NO: 6:	
GCTGCTTGGG GACTGGG	TCA GCTGGAT		27
(2)	INFORMATION FOR	SEQ ID NO: 7:	
(i)	SEQUENCE CHARACT	TERISTICS:	
	(A) LENGTH: 21	bases	
	(B) TYPE: nucl	leic acid	

. 4

single

(C) STRANDEDNESS:

(ii)	MOLECULE TYPE: oligonucleotide	
(ix)	FEATURE:	
	(A) NAME/KEY: PCR primer	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 7:	
ATTCAGCTGA CCCAGT	CTCC A	21
(2)	INFORMATION FOR SEQ ID NO: 8:	
(i)	SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 58 bases	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: oligonucleotide	
(ix)	FEATURE:	
	(A) NAME/KEY: PCR primer	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 8:	
GATCGGATCC ACCTGA	GGAA GCAAAGTTTA AATTCTACTC ACGTTTCAGT TCCAGCTT	58
(2)	INFORMATION FOR SEQ ID NO: 9:	
(i)	SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 31 bases	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	

(D) TOPOLOGY: linear

(D) TOPOLOGY: linear (ii) MOLECULE TYPE: oligonucleotide (ix) FEATURE: (A) NAME/KEY: PCR primer (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9: TCTCCTGCAG TGGGACCTCG GAGTGGACAC C 31 (2) INFORMATION FOR SEQ ID NO: 10: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 21 bases (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: oligonucleotide (ix) FEATURE: NAME/KEY: PCR primer (A) (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10: GAGGTCCAGC TGCAGCAGTC T 21 (2) INFORMATION FOR SEQ ID NO: 11: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 24 bases

TYPE: nucleic acid

STRANDEDNESS: single

(B)

(C)

(D) TOPOLOGY: linear (ii) MOLECULE TYPE: oligonucleotide (ix) FEATURE: (A) NAME/KEY: PCR primer (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11: CGATGTATCA GCTGTCAGTG TGGC 24 (2) INFORMATION FOR SEQ ID NO: 12: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 24 bases (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: oligonucleotide (ix) FEATURE: (A) NAME/KEY: PCR primer (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12: GCCACACTGA CAGCTGATAC ATCG 24 (2) INFORMATION FOR SEQ ID NO: 13: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 21 bases (B) TYPE: nucleic acid

STRANDEDNESS: single

(C)

- (D) TOPOLOGY: linear (ii) MOLECULE TYPE: oligonucleotide (ix) FEATURE: (A) NAME/KEY: PCR primer (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13: CAGAGTGCCT TGGCCCCAGT A 21 (2) INFORMATION FOR SEQ ID NO: 14: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 27 bases (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: oligonucleotide (ix) FEATURE: NAME/KEY: PCR primer (A) (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14: TACTGGGGCC AAGGCACCCT CGTCACA 27
  - (2) INFORMATION FOR SEQ ID NO: 15:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 25 bases
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: oligonucleotide
- (ix) FEATURE:
  - (A) NAME/KEY: PCR primer
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

GATCGGATCC CTATAAATCT CTGGC

25

- (2) INFORMATION FOR SEQ ID NO: 16:
- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 43 bases
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: oligonucleotide
- (ix) FEATURE:
  - (A) NAME/KEY: PCR primer
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

TTGGATCCGC GGCCGCGTCG ACTACAGTTG GTGCAGCATC AGC

- (2) INFORMATION FOR SEQ ID NO: 17:
- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 41 bases
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: oligonucleotide
- (ix) FEATURE:
  - (A) NAME/KEY: PCR primer
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

ATGGATCCGC GGCCGCGTCG ACCCAGTGGA TAGACCGATG G

41

- (2) INFORMATION FOR SEQ ID NO: 18:
- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 31 bases
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: oligonucleotide
- (ix) FEATURE:
  - (A) NAME/KEY: PCR primer
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:
  - (2) INFORMATION FOR SEQ ID NO: 19:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 29 bases
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single

- (D) TOPOLOGY: linear (ii) MOLECULE TYPE: oligonucleotide (ix) FEATURE: (A) NAME/KEY: PCR primer (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19: CCTGTTTAGG CCTCTGCTTC ACCCAGTAC 29 (2) INFORMATION FOR SEQ ID NO: 20: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 29 bases (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: oligonucleotide (ix) FEATURE: NAME/KEY: PCR primer (A) (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20: GGATAATGGG TAAATTGCAT GCAGTAATA 29
  - (2) INFORMATION FOR SEQ ID NO: 21:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 30 bases
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear (ii) MOLECULE TYPE: oligonucleotide (ix) FEATURE: (A) NAME/KEY: PCR primer (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21: TGCAAGCTTC ATGATGAGTC CTGTCCAGTC 30 (2) INFORMATION FOR SEQ ID NO: 22: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 28 bases (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: oligonucleotide (ix) FEATURE: (A) NAME/KEY: PCR primer (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22: AGTAAGCTTC ATGAAATGCA GGTGGATC 28

- (2) INFORMATION FOR SEQ ID NO: 23:
- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 bases
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single

(	ii)	MOLECULE TYPE: oligonucleotide	
· (	ix)	FEATURE:	
		(A) NAME/KEY: PCR primer	
(	xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 23:	
GGGAGATTGC TGC	CAGCTO	GGA CTTC	24
(	(2)	INFORMATION FOR SEQ ID NO: 24:	
(	(i)	SEQUENCE CHARACTERISTICS:	
		(A) LENGTH: 33 bases	
		(B) TYPE: nucleic acid	
		(C) STRANDEDNESS: single	
		(D) TOPOLOGY: linear	
(	ii)	MOLECULE TYPE: oligonucleotide	
(	ix)	FEATURE:	
		(A) NAME/KEY: PCR primer	
(	xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 24:	
GATCCCCGGG CCA	CCATO	GAT GAGTCCTGTC CAG	33
(	2)	INFORMATION FOR SEQ ID NO: 25:	
(	i)	SEQUENCE CHARACTERISTICS:	
		(A) LENGTH: 61 bases	
		(B) TYPE: nucleic acid	
		(C) STRANDEDNESS: single	
		(D) TOPOLOGY: linear	

(D) TOPOLOGY: linear

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(ix)	FEATURE:	
	(A) NAME/KEY: PCR primer	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 25:	
AGAATGGCCA CGTCATC	CCGA CCCCCTCAGA GTTTACTATT CTACTATCCA ACTGAGGAAG	60
С		61
(2)	INFORMATION FOR SEQ ID NO: 26:	
(i)	SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 34 bases	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: oligonucleotide	
(ix)	FEATURE:	
	(A) NAME/KEY: PCR primer	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 26:	
GATCGAATTC GCCACCA	TGA AATGCAGGTG GATC	34
(2)	INFORMATION FOR SEQ ID NO: 27:	
(i)	SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 37 bases	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	

(ii) MOLECULE TYPE: oligonucleotide

(D) TOPOLOGY: linear

(A) NAME/KEY: PCR primer (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27: CCAGAAAGCT AGCTTGCCAT CCCTATAAAT CTCTGGC 37 (2) INFORMATION FOR SEQ ID NO: 28: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 23 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: polypeptide (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28: Asp Val Val Leu Thr Gln Thr Pro Pro Thr · 5 Leu Leu Ala Thr Ile Gly Gln Ser Val Ser 15 20 Ile Ser Cys (2) INFORMATION FOR SEQ ID NO: 29: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 23 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

(ix) FEATURE:

(ii) MOLECULE TYPE: polypeptide (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29: Asp Val Val Met Thr Gln Ser Pro Leu Ser 5 10 Leu Pro Val Thr Leu Gly Gln Pro Ala Ser 20 15 Ile Ser Cys INFORMATION FOR SEQ ID NO: 30: (2) (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 15 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: polypeptide (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30: Trp Leu Leu Gln Arg Thr Gly Gln Ser Pro 5 10 Gln Pro Leu Ile Tyr 15 (2) INFORMATION FOR SEQ ID NO: 31: (i) SEQUENCE CHARACTERISTICS: LENGTH: 15 amino acids (A) (B) TYPE: amino acid (C) STRANDEDNESS:

				(D)	TOP	OLOGY	<i>:</i>	linea	r			
		(i	i) ľ	MOLE	CULE	TYPE	3:	polyp	epti	de		
		(x	i) \$	SEQUI	ENCE	DESC	CRIP	TION:	SE	Q ID	NO:	31:
Trp	Phe	Gln	Gln	Arg	Pro	Gly	Gln	Ser	Pro			
				5					10			
Arg	Arg	Leu	Ile	Tyr								
				15								
(2)		IN	FORI	OITAN	ON FO	OR SI	EQ I	D NO:	32:			
		(i	) 8	SEQUI	ENCE	CHAI	RACT	ERIST	CICS:			
				(A)	LEN	GTH:	32	amino	aci	ds		
				(B)	TYPI	3: a	amin	o aci	.d			
				(C)	STRA	ANDEI	ONES	S:				
				(D)	TOPO	OLOGY	<i>t</i> :	linea	.r			
		(i	i) ľ	MOLEC	CULE	TYPE	€:	polyp	epti	lе		
		(x	i) S	SEQUE	ENCE	DESC	CRIP	TION:	SE	OI C	NO:	32:
Gly	Val	Pro .	Asn	Arg	Phe	Ser	Gly	Ser	Gly			
				5					10			
Ser	Gly	Thr .	Asp	Phe	Thr	Leu	Lys	Ile	Ser			
				15					20			
Gly	Val	Glu 2	Ala	Glu	Asp	Leu	Gly	Val	Tyr			
		•		25					30			
Tyr	Cys											
(2)		IN	FORM	OITA	N FO	R SE	Q I	D NO:	33:			

(i) SEQUENCE CHARACTERISTICS:

(11) 22101111 32 411110 40140
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: polypeptide
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:
Gly Val Pro Asp Arg Phe Ser Gly Ser Gly
5 10
Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser
15 20
Arg Val Glu Ala Glu Asp Val Gly Val Tyr
25 30
Tyr Cys
(2) INFORMATION FOR SEQ ID NO: 34:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: polypeptide
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:
Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys
5 10

(A) LENGTH: 32 amino acids

(2) INFORMATION FOR SEQ ID NO: 35:

(A) LENGTH: 10 amino acids	
(B) TYPE: amino acid	
(C) STRANDEDNESS:	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: polypeptide	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:	
Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys	
5 10	
(2) INFORMATION FOR SEQ ID NO: 36:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 81 bases	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: oligonucleotide	
(ix) FEATURE:	
(A) NAME/KEY: PCR primer	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:	
GCAAGAGATG GAAGCTGGTT GTCCCAAGGT TACCAATAAT GAAGGTGGAC TCTGGGTCAT	60
CACAACATCA CCATTGGTTC C	81
(2) INFORMATION FOR SEQ ID NO: 37:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 72 bases	

(i) SEQUENCE CHARACTERISTICS:

	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
t)	ii) MOLECULE TYPE: oligonucleotide	
t)	ix) FEATURE:	
	(A) NAME/KEY: PCR primer	
(2	xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:	
CAACCAGCTT CCAT	TCTCTTG CAGGTCAAGT CAGAGTCTCT TACATAGTAG TGGAAACACC	60
TATTTAAATT GG		72
(2) II	NFORMATION FOR SEQ ID NO: 38:	
(i)	i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 81 bases	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
i)	ii) MOLECULE TYPE: oligonucleotide	
i)	ix) FEATURE:	
	(A) NAME/KEY: PCR primer	
к)	ki) SEQUENCE DESCRIPTION: SEQ ID NO: 38:	
AGATTCCAGT TTGG	GATACCA AATAAATTAG CGGCTGTGGA GATTGGCCTG GCCTTAGCAA	50
CCAATTTAAA TAGG	GTGTTTC C	31
(2) IN	NFORMATION FOR SEQ ID NO: 39:	
(i	E) SEQUENCE CHARACTERISTICS:	

LENGTH: 81 bases

(A)

(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: oligonucleotide	
(ix) FEATURE:	
(A) NAME/KEY: PCR primer	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:	
TTGGTATCCA AACTGGAATC TGGGGTCCCC GACAGGTTCA GTGGCTCAGG GAGTGGAACA	0
GATTTCACAC TCAAAATCAG T	31
(2) INFORMATION FOR SEQ ID NO: 40:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 72 bases	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: oligonucleotide	
(ix) FEATURE:	
(A) NAME/KEY: PCR primer	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:	
TGGGTAAAT TGCATGCAGT AATAAACCCC CACATCCTCA GCTTCCACTC CACTGATTTT 6	0
AGTGTGAAA TC	2
2) INFORMATION FOR SEQ ID NO: 41:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 63 bases	

		(b) TIPE: Mucleic acid	
		(C) STRANDEDNESS: single	
		(D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: oligonucleotide	
	(ix)	FEATURE:	
		(A) NAME/KEY: PCR primer	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 41:	
TACTGCATGC A	ATTTAC	CCA TTATCCGTAC ACGTTTGGAC AAGGGACCAA GCTGGAAATC	60
AAA			63
(2)	INFO	RMATION FOR SEQ ID NO: 42:	
	(i)	SEQUENCE CHARACTERISTICS:	
		(A) LENGTH: 67 bases	
		(B) TYPE: nucleic acid	
		(C) STRANDEDNESS: single	
		(D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: oligonucleotide	
	(ix)	FEATURE:	
		(A) NAME/KEY: PCR primer	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 42:	
GATCGGATCC A	ACTGAG	GAA GCAAAGTTTA AATTCTACTC ACGTTTGATT TCCAGCTTGG	60
TCCCTTG			67
(2)	INFO	RMATION FOR SEQ ID NO: 43:	
	(i)	SEQUENCE CHARACTERISTICS:	
		(A) LENGTH: 23 bases	

		(C) STRANDEDNESS: single	
		(D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: oligonucleotide	
	(ix)	FEATURE:	
		(A) NAME/KEY: PCR primer	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 43:	
GATCAAGCTT C	ATGATG	AGT CCT	23
	•		
(2)	INFO	RMATION FOR SEQ ID NO: 44:	
	(i)	SEQUENCE CHARACTERISTICS:	
		(A) LENGTH: 21 bases	
		(B) TYPE: nucleic acid	
		(C) STRANDEDNESS: single	
		(D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: oligonucleotide	
	(ix)	FEATURE:	
		(A) NAME/KEY: PCR primer	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 44:	
GCAAGAGATG G	AAGCTG	GTT G	21
(2)	INFO	RMATION FOR SEQ ID NO: 45:	
	(i)	SEQUENCE CHARACTERISTICS:	
		(A) LENGTH: 21 bases	
		(B) TYPE: nucleic acid	
		(C) STRANDEDNESS: single	

(B) TYPE: nucleic acid

	(ii)	MOLECULE TYPE: oligonucleotide	
	(ix)	FEATURE:	
		(A) NAME/KEY: PCR primer	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 45:	
CAACCAGCTT C	CATCTC	CTTG C	21
(2)	INFO	RMATION FOR SEQ ID NO: 46:	
	(i)	SEQUENCE CHARACTERISTICS:	
		(A) LENGTH: 21 bases	
		(B) TYPE: nucleic acid	
		(C) STRANDEDNESS: single	
		(D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: oligonucleotide	
	(ix)	FEATURE:	
		(A) NAME/KEY: PCR primer	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 46:	
AGATTCCAGT T	TGGATA	ACCA A	21
(2)	INFO	RMATION FOR SEQ ID NO: 47:	
	(i)	SEQUENCE CHARACTERISTICS:	
		(A) LENGTH: 24 bases	
		(B) TYPE: nucleic acid	
		(C) STRANDEDNESS: single	
		(D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: oligonucleotide	

TOPOLOGY:

(D)

linear

	(ix)	FEATURE:	
		(A) NAME/KEY: PCR primer	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 47:	
TTGGTATCCA A	ACTGGA	ATC TGGG	24
(2)	INFO	RMATION FOR SEQ ID NO: 48:	
	(i)	SEQUENCE CHARACTERISTICS:	
		(A) LENGTH: 24 bases	
		(B) TYPE: nucleic acid	
		(C) STRANDEDNESS: single	
		(D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: oligonucleotide	
	(ix)	FEATURE:	
		(A) NAME/KEY: PCR primer	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 48:	
ATGGGTAAAT T	GCATGC	AGT AATA	24
(2)	INFO	RMATION FOR SEQ ID NO: 49:	
	(i)	SEQUENCE CHARACTERISTICS:	
		(A) LENGTH: 24 bases	
		(B) TYPE: nucleic acid	
		(C) STRANDEDNESS: single	
		(D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: oligonucleotide	
	(ix)	FEATURE:	
		(A) NAME/KEY: PCR primer	

	(X1)	SEQUENCE DESCRIPTION: SEQ ID NO: 49:	
TACTGCAT	GC AATTTAC	CCA TTAT	24
(0)			
(2)	INFO	RMATION FOR SEQ ID NO: 50:	
	(i)	SEQUENCE CHARACTERISTICS:	
		(A) LENGTH: 26 bases	
		(B) TYPE: nucleic acid	
		(C) STRANDEDNESS: single	
		(D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: oligonucleotide	
	(ix)	FEATURE:	
		(A) NAME/KEY: PCR primer	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 50:	
GATCGGATC	C AACTGAG	GAA GCAAAG	26
(2)	INFOR	RMATION FOR SEQ ID NO: 51:	
	(i)	SEQUENCE CHARACTERISTICS:	
		(A) LENGTH: 30 amino acids	
		(B) TYPE: amino acid	
		(C) STRANDEDNESS:	
		(D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: polypeptide	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 51:	
Glu Val	Gln Leu	Gln Gln Ser Gly Pro Glu	
		5 10	
Leu Gla	Ara Pro	Gly Ala Sar Val Lyg Lau	

Ser	Cys	Lys Al	a Ser	Gly Tyr Ile Phe Thr	
			25	30	
(2)		INFO	RMATI	ON FOR SEQ ID NO: 52:	
		(i)	SEQU	JENCE CHARACTERISTICS:	
			(A)	LENGTH: 30 amino acids	
			(B)	TYPE: amino acid	
			(C)	STRANDEDNESS:	
			(D)	TOPOLOGY: linear	
		(ii)	MOLE	CULE TYPE: polypeptide	
		(xi)	SEQUI	ENCE DESCRIPTION: SEQ ID NO: 52	:
Gln	Val	Gln Le	u Val	Gln Ser Gly Ala Glu	
			5	10	
Val	Lys	Lys Pr	o Gly	Ala Ser Val Lys Val	
			15	20	
Ser	Cys	Lys Al	a Ser	Gly Tyr Thr Phe Thr	
			25	30	
(2)		INFO	RMATIC	ON FOR SEQ ID NO: 53:	
		(i)	SEQUE	ENCE CHARACTERISTICS:	
			(A)	LENGTH: 14 amino acids	
			(B)	TYPE: amino acid	
			(C)	STRANDEDNESS:	
			(D)	TOPOLOGY: linear	
		(ii)	MOLEC	CULE TYPE: polypeptide	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:
Trp Val Lys Gln Arg Pro Lys Gln Gly Leu

5 10

Glu Leu Val Gly

- (2) INFORMATION FOR SEQ ID NO: 54:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 14 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: polypeptide
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

Trp Val Arg Gln Ala Pro Gly Gln Gly Leu

5 10

Glu Trp Met Gly

- (2) INFORMATION FOR SEQ ID NO: 55:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 32 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: polypeptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:
  Lys Ala Thr Leu Thr Ala Asp Thr Ser Ser

			5					10		
Asn	Thr	Ala T	Tyr Met	Gln	Leu	Ser	Ser	Leu		
			15					20		
Thr	Ser	Glu A	Asp Thr	Ala	Thr	Tyr	Phe	Cys		
			25					30		
Ala	Arg									
(2)		INF	ORMATIC	ON FO	OR SE	EQ II	NO:	56:		
		(i)	SEQUE	ENCE	CHAI	RACTI	ERIST	CICS:		
			(A)	LENC	GTH:	32 a	mino	acids	3	
			(B)	TYPI	∃: a	amino	aci	ld		
			(C)	STRA	ANDEI	NESS	<b>:</b>			
			(D)	TOPO	OLOGY	<b>7:</b> 1	inea	ır		
		(ii	) MOLEC	CULE	TYPE	E: p	olyr	eptide	<b>&gt;</b>	
		(xi	.) SEQUE	ENCE	DESC	RIPT	'ION:	SEQ	ID NO	: 56:
Arg	Val	Thr M	Met Thr	Arg	Asp	Thr	Ser	Ile		
			5					10		
Ser	Thr	Ala T	Tyr Met	Glu	Leu	Ser	Arg	Leu		
			15					20		
Arg	Ser	Asp A	sp Thr	Ala	Val	Tyr	Tyr	Cys		
			25					30		
Ala	Arg									
(2)		INF	ORMATIC	N FC	R SE	Q ID	NO:	57:		
		(i)	SEQUE	ENCE	CHAR	ACTE	RIST	'ICS:		
			(A)	LENG	TH:	11 a	mino	acids	}	

	(D	TOPOLOGY	: linear			
	(ii) MO	LECULE TYPE	: polyper	ptide		
	(xi) SE	QUENCE DESC	RIPTION:	SEQ ID	NO:	57:
Trp	Gly Gln Gly T	hr Leu Val	Thr Val Se	er		
		5	:	10		
Ser						
(2)	INFORMA	TION FOR SE	Q ID NO:	58:		
	(i) SE	QUENCE CHAR	ACTERISTI	CS:		
	(A	) LENGTH:	11 amino a	acids		
	(B	) TYPE: a	mino acid			
	(C	) STRANDED	NESS:			
	(D	) TOPOLOGY	: linear			
	(ii) MO	LECULE TYPE	: polype	otide		
	(xi) SE	QUENCE DESC	RIPTION:	SEQ ID	NO:	58:
Trp	Gly Gln Gly T	hr Leu Val	Thr Val Se	er		
		5	:	10		
Ser						
(2)		TION FOR SE				
		QUENCE CHAR		CS:		
	·	) LENGTH:				
		) TYPE: n				
	(C	) STRANDED	NESS: sir	ngle		

TYPE: amino acid

(C) STRANDEDNESS:

(B)

(i	i) MOLECULE TYPE: oligonucleotide	
(i	x) FEATURE:	
	(A) NAME/KEY: PCR primer	
( <b>x</b>	i) SEQUENCE DESCRIPTION: SEQ ID NO: 59:	
GATCAAGCTT CATG	AAATGC AGGTGGATCA TCCTCTTCTT GATGGCAGTA GCTACAGGTA	60
AGGCACTCCC AAGT	CGTAAA CTTGAGAG	88
(2) IN	FORMATION FOR SEQ ID NO: 60:	
(i	.) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 87 bases	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
(i	i) MOLECULE TYPE: oligonucleotide	
(i	x) FEATURE:	
	(A) NAME/KEY: PCR primer	
(x	i) SEQUENCE DESCRIPTION: SEQ ID NO: 60:	
CACCTGTGAG TTGA	CCCCTG TTGAAAGAAA TCCAAAGATA GTGTCACTGT CTCCCAAGTG	50
TATGATCTCT CAAG	TTTAGG ACTTGGG	37
(2) IN	FORMATION FOR SEQ ID NO: 61:	
(i	) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 78 bases	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	

(D) TOPOLOGY: linear

	(D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: oligonucleotide	
(ix)	FEATURE:	
	(A) NAME/KEY: PCR primer	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 61:	
ACAGGGGTCA ACTCACA	GGT GCAGCTGGTG CAGTCTGGGG CTGAGGTGAA GAAGCCTGGG	60
GCCTCAGTGA AGGTCTC	ec ·	78
(2) INFO	RMATION FOR SEQ ID NO: 62:	
(i)	SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 78 bases	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: oligonucleotide	
(ix)	FEATURE:	
	(A) NAME/KEY: PCR primer	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 62:	
GGCCTGTCGC ACCCAGT	ACA TATAGTACTC GGTGAAGGTG TATCCAGAAG CCTTGCAGGA	60
GACCTTCACT GAGGCCC	ec e e e e e e e e e e e e e e e e e e	78
(2) INFO	RMATION FOR SEQ ID NO: 63:	
(i)	SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 78 bases	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	

	(D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: oligonucleotide	
(ix)	FEATURE:	
	(A) NAME/KEY: PCR primer	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 63:	
ATGTACTGGG TGCGACA	AGGC CCCTGGACAA GGGCTTGAGC TGATGGGAAG GATCGATCCT	60
GAAGACGGTA GTATTGA	AT .	78
(2) INFO	RMATION FOR SEQ ID NO: 64:	
(i)	SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 78 bases	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: oligonucleotide	
(ix)	FEATURE:	
	(A) NAME/KEY: PCR primer	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 64:	
TGTGCTAGAG GACGTGT	CAG CGGTCAGGGT GACCTTTTC TTAAACTTCT CAACATAATC	60
AATACTACCG TCTTCAG	GG C	78
(2) INFO	RMATION FOR SEQ ID NO: 65:	
(i)	SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 84 bases	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	

(ii) Mo	OLECULE TYPE: oligonucleotide	
(ix) F	EATURE:	
(2	A) NAME/KEY: PCR primer	
(xi) S	EQUENCE DESCRIPTION: SEQ ID NO: 65:	
GCTGACACGT CCTCTAGCA	C AGCCTACATG GAGCTGAGCA GCCTGACCTC TGACGACACG	60
GCCGTGTATT ACTGTGCGA	G AGGA	84
(2) INFORM	ATION FOR SEQ ID NO: 66:	
(i) S	EQUENCE CHARACTERISTICS:	
(.	A) LENGTH: 87 bases	
(	B) TYPE: nucleic acid	
(	C) STRANDEDNESS: single	
(	D) TOPOLOGY: linear	
(ii) · M	OLECULE TYPE: oligonucleotide	
(ix) F	EATURE:	
. (	A) NAME/KEY: PCR primer	
(xi) S	EQUENCE DESCRIPTION: SEQ ID NO: 66:	
GGACTCACCT GAGGAGACG	G TGACCAGGGT TCCTTGGCCC CAGTAAGCAA ACCTATAGTT	60
AAACTTTCCT CTCGCACAG	T AATACAC	87
(2) INFORM	ATION FOR SEQ ID NO: 67:	
(i) S	EQUENCE CHARACTERISTICS:	
(.	A) LENGTH: 69 bases	
(	B) TYPE: nucleic acid	
(	C) STRANDEDNESS: single	

(D) TOPOLOGY: linear

		(D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: oligonucleotide	
	(ix)	FEATURE:	
		(A) NAME/KEY: PCR primer	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 67:	
ACCGTCTCCT C	AGGTGA	GTC CTTACAACCT CTCTCTTCTA TTCAGCTTAA ATAGATTTTA	60
CTGCATTTG			69
(2)	INFO	RMATION FOR SEQ ID NO: 68:	
	(i)	SEQUENCE CHARACTERISTICS:	
		(A) LENGTH: 69 bases	
		(B) TYPE: nucleic acid	
		(C) STRANDEDNESS: single	
		(D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: oligonucleotide	
	(ix)	FEATURE:	
		(A) NAME/KEY: PCR primer	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 68:	
CCTAGTCCTT CA	ATGACC'	TGA AATTCAGATA CACACATTTC CCCCCCAACA AATGCAGTAA	60
AATCTATTT			69
(2)	INFOR	RMATION FOR SEQ ID NO: 69:	
	(i)	SEQUENCE CHARACTERISTICS:	
		(A) LENGTH: 72 bases	
		(B) TYPE: nucleic acid	
		(C) STRANDEDNESS: single	

		(D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: oligon	ucleotide
	(ix)	FEATURE:	
		(A) NAME/KEY: PCR pr	imer
	(xi)	SEQUENCE DESCRIPTION:	SEQ ID NO: 69:
TTCAGGTCAT G	AAGGAC	TAG GGACACCTTG GGAGTCAGAA AGG	GTCATTG GGAGCCCGGG 60
CTGATGCAGA C	A.		72
(2)	INFO	RMATION FOR SEQ ID NO:	70:
	(i)	SEQUENCE CHARACTERISTI	CS:
		(A) LENGTH: 72 bases	
		(B) TYPE: nucleic ac	id
		(C) STRANDEDNESS: si	ngle
		(D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: oligon	ucleotide
	(ix)	FEATURE:	
		(A) NAME/KEY: PCR pr	imer
	(xi)	SEQUENCE DESCRIPTION:	SEQ ID NO: 70:
GATCGGATCC C	TATAAA	ICT CTGGCCATGA AGTCTGGGAG CTG	AGGATGT CTGTCTGCAT 60
CAGCCCGGGC TO	C		72
(2)	INFO	RMATION FOR SEQ ID NO:	71:
	(i)	SEQUENCE CHARACTERISTIC	CS:
		(A) LENGTH: 25 bases	
		(B) TYPE: nucleic ac	id
		(C) STRANDEDNESS: si	nale

		(b) Toponogi: Timear	
	(ii)	MOLECULE TYPE: oligonucleotide	
	(ix)	FEATURE:	
		(A) NAME/KEY: PCR primer	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 71:	
GATCAAGCTT C	ATGAAA	TGC AGGTG	25
(2)	INFO	RMATION FOR SEQ ID NO: 72:	
	(i)	SEQUENCE CHARACTERISTICS:	
		(A) LENGTH: 23 bases	
		(B) TYPE: nucleic acid	
		(C) STRANDEDNESS: single	
		(D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: oligonucleotide	
	(ix)	FEATURE:	
		(A) NAME/KEY: PCR primer	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 72:	
CACCTGTGAG T	TGACCC	CTG TTG	23
(2)	INFOR	RMATION FOR SEQ ID NO: 73:	
	(i)	SEQUENCE CHARACTERISTICS:	
		(A) LENGTH: 21 bases	
		(B) TYPE: nucleic acid	
		(C) STRANDEDNESS: single	
		(D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: oligonucleotide	

	(ix)	FEATURE:	
		(A) NAME/KEY: PCR primer	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 73:	
ACAGGGGTCA A	CTCACA	GGT G	21
(2)	INFO	RMATION FOR SEQ ID NO: 74:	
	(i)	SEQUENCE CHARACTERISTICS:	
		(A) LENGTH: 21 bases	
		(B) TYPE: nucleic acid	
		(C) STRANDEDNESS: single	
		(D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: oligonucleotide	
	(ix)	FEATURE:	
		(A) NAME/KEY: PCR primer	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 74:	
GGCCTGTCGC A	CCCAGT.	ACA T	21
(2)	INFO	RMATION FOR SEQ ID NO: 75:	
	(i)	SEQUENCE CHARACTERISTICS:	
		(A) LENGTH: 21 bases	
		(B) TYPE: nucleic acid	
		(C) STRANDEDNESS: single	
		(D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: oligonucleotide	
	(ix)	FEATURE:	
		(A) NAME/KEY: PCR primer	

	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 75:	
ATGTACTGGG '	TGCGACA	GGC C	21
(2)	INFO	RMATION FOR SEQ ID NO: 76:	
	(i)	SEQUENCE CHARACTERISTICS:	
		(A) LENGTH: 21 bases	
		(B) TYPE: nucleic acid	
		(C) STRANDEDNESS: single	
		(D) TOPOLOGY: linear	
	/ii\	MOLECULE TYPE: oligonucleotide	
		•	
	(ix)	FEATURE:	
		(A) NAME/KEY: PCR primer	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 76:	
TGTGCTAGAG	GACGTGT	'CAG C	21
(2)	INFO	RMATION FOR SEQ ID NO: 77:	
	(i)	SEQUENCE CHARACTERISTICS:	
		(A) LENGTH: 21 bases	
		(B) TYPE: nucleic acid	
		(C) STRANDEDNESS: single	
		(D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: oligonucleotide	
	(ix)	FEATURE:	
		(A) NAME/KEY: PCR primer	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 77:	
GCTGACACGT	CCTCTAG	CAC A	21

(2)	INFORMATION	N FOR SEQ ID NO: 78:	
	(i) SEQUEN	NCE CHARACTERISTICS:	
	(A) I	LENGTH: 21 bases	
	(B) T	TYPE: nucleic acid	
	(C) S	STRANDEDNESS: single	
	(D) T	TOPOLOGY: linear	
	(ii) MOLECU	JLE TYPE: oligonucleotide	
	(ix) FEATUR	₹E:	
	(A) N	NAME/KEY: PCR primer	
	(xi) SEQUEN	NCE DESCRIPTION: SEQ ID NO: 78:	
GGACTCACCT	GAGGAGACGG T		21
(2)	INFORMATION	N FOR SEQ ID NO: 79:	
	(i) SEQUEN	NCE CHARACTERISTICS:	
	(A) L	ENGTH: 21 bases	
	(B) I	TYPE: nucleic acid	
	(C) S	STRANDEDNESS: single	
	(D) T	COPOLOGY: linear	
	(ii) MOLECU	LE TYPE: oligonucleotide	
	(ix) FEATUR	E:	
	(A) N	IAME/KEY: PCR primer	
	(xi) SEQUEN	ICE DESCRIPTION: SEQ ID NO: 79:	
ACCGTCTCCT	CAGGTGAGTC C		21

INFORMATION FOR SEQ ID NO: 80:

(2)

	(i)	SEQUENCE CHARACTERISTICS:	
		(A) LENGTH: 21 bases	
		(B) TYPE: nucleic acid	
	٠	(C) STRANDEDNESS: single	
		(D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: oligonucleotide	
	(ix)	FEATURE:	
		(A) NAME/KEY: PCR primer	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 80:	
CCTAGTCCTT C	ATGACC	TGA A	21
(2)	INFO	RMATION FOR SEQ ID NO: 81:	
	(i)	SEQUENCE CHARACTERISTICS:	
		(A) LENGTH: 21 bases	
		(B) TYPE: nucleic acid	
		(C) STRANDEDNESS: single	
		(D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: oligonucleotide	
	(ix)	FEATURE:	
		(A) NAME/KEY: PCR primer	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO: 81:	
TTCAGGTCAT G	AACGAC'	TAG G	21
(2)	INFOR	RMATION FOR SEQ ID NO: 82:	
	(i)	SEQUENCE CHARACTERISTICS:	

(A) LENGTH: 26 bases

		(D)	TOPOLOGY:	linear		•
	(ii)	MOLE	CULE TYPE:	oligonucleot	ide	
	(ix)	FEAT	JRE:			
		(A)	NAME/KEY:	PCR primer		
	(xi)	SEQUE	ENCE DESCRIP	TION: SEQ I	D NO: 82:	
GATCGGATCC C	TATAAA'	TCT CTC	egcc			26
(2)	INFO	TAMS	ON FOR SEQ I	D NO: 83:		
	(i)	SEQUE	ENCE CHARACT	ERISTICS:		
		(A)	LENGTH: 761	bases		
		(B)	TYPE: nucl	eic acid		
		(C)	STRANDEDNES	S: single		
		(D)	TOPOLOGY:	linear		
	(ii)	MOLE	CULE TYPE:	oligonucleot	ide	
	(ix)	FEAT	JRE:			
		(A)	NAME/KEY:	Nucleotide	sequence	encoding LO-
CD2a V <sub>L</sub> cha	ain.					
	(xi)	SEQUE	NCE DESCRIP	TION: SEQ I	D NO: 83:	
ATGATGAGTC C	TGTCCA	TC CCI	GTTTCTG TTATTG	CTTT GGATTCTGGG	TAAGTAGAGA	60
ATGAGTTACA G	GACAAGA	AAT GGG	GATGGAG GATGAG	TTCT GACTGCCCAT	GTTGGCTGTC	120
CATGTGTGGT A	AGGCAGG	TC CTA	TTTTCTA AGATGG	ACAC TTGAGATTCC	ATTACTTGAT	180
AATGAGAAAT T	ACAGATO	GAG ATA	GGATTTG TGCTAA	GAGG ATTCTAATGT	AGATGAGAAG	240
GTGTATGCCA T	TTAGGAT	CT GCA	ACCGAAT TGTTTT	GTGA AAAAGCATTT	GGTATATTTT	300
ттааааатса с	AAAACA	CAC CGG	GATCTCA CAGGAA	ATGA GTAACAAAA	GTAATTCACA	360

TYPE: nucleic acid

(C) STRANDEDNESS: single

(B)

AAGATTGGTT	GCAAATTTTG	CACATAACTI	TGTTCTGATC	TATTATAATT	TCAGGAACCA	420
ATGGTGATGT	TGTGCTGACC	CAGACTCCAC	CTACTTTATT	GGCTACCATT	GGACAATCAG	480
TCTCCATCTC	TTGCAGGTCA	AGTCAGAGTC	TCTTACATAG	TAGTGGAAAC	ACCTATTTAA	540
ATTGGTTGCT	ACAGAGGACA	GGCCAATCTC	CACAGCCGCT	AATTTATTTG	GTATCCAAAC	600
TGGAATCTGG	GGTCCCCAAC	AGGTTCAGTG	GCAGTGGGTC	AGGAACAGAT	TTCACACTCA	660
AAATCAGTGG	AGTGGAAGCT	GAGGATTTGG	GGGTTTATTA	CTGCATGCAA	TTTACCCATT	720
ATCCGTACAC	GTTTGGAGCT	GGGACCAAGC	TGGAACTGAA	A		761

## (2) INFORMATION FOR SEQ ID NO: 84:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 132 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: polypeptide
- (ix) FEATURE:
  - (A) NAME/KEY: Chimeric LO-CD2a V<sub>L</sub> Chain
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:

Met Met Ser Pro Val Gln Ser Leu Phe

-20 -15

Leu Leu Leu Trp Ile Leu Gly Thr Asn

-10 -5

Gly Asp Val Val Leu Thr Gln Thr Pro

-1 +1

Pro Thr Leu Leu Ala Thr Ile Gly Gln Ser

	10					15				
Val	Ser	Ile	Ser	Cys	Arg	Ser	Ser	Gln	Ser	Leu
	20					25				
Leu	His	Ser	Ser	Gly	Asn	Thr	Tyr	Leu	Asn	Trp
30					35					40
Leu	Leu	Gln	Arg	Thr	Gly	Gln	Ser	Pro	Gln	
				45					50	
Pro	Leu	Ile	Tyr	Leu	Val	Ser	Lys	Leu	Glu	
				55					60	
Ser	Gly	Val	Pro	Asn	Arg	Phe	Ser	Gly	Ser	
				65					70	
Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Lys	Ile	
				75					80	
Ser	Gly	Val	Glu	Ala	Glu	Asp	Leu	Gly	Val	
				85					90	
Tyr	Tyr	Cys	Met	Gln	Phe	Thr	His	Tyr	Pro	
				95					100	
Tyr	Thr	Phe	Gly	Ala	Gly	Thr	Lys	Leu	Glu	
				105					110	
Leu	Lys									
(2)		IN	IFORM	IATIC	ON FO	OR SE	EQ II	NO:	85:	
		(i	.) .5	EQUE	ENCE	CHAR	RACTE	ERIST	CICS:	
			(	(A)	LENG	TH:	491	base	s	
			(	(B)	TYPE	: n	ucle	ic a	cid	
			(	(C)	STRA	NDED	NESS	: s	ingl	е
			(	D)	TOPO	LOGY	: 1	inea	r	

- (ii) MOLECULE TYPE: oligonucleotide
- (ix) FEATURE:
- (A) NAME/KEY: Nucleotide sequence encoding LO-CD2a  $V_{\scriptscriptstyle H}$  chain.
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85: ATGAAATGCA GGTGGATCAT CCTCTTCTTG ATGGCAGTAG CTACAGGTAA GGCACTCCCA 60 AGTCCTAAAC TTGAGAGATC ATACACTTGG GAGACAGTGA CACTATCTTT GGATTTCTTT 120 CAACAGGGGT CAACTCAGAA GTCCAGCTGC AGCAATCTGG GCCTGAGCTT CAGAGACCCG 180 GGGCCTCAGT CAAGTTGTCG TGCAAGGCTT CTGGCTATAT ATTTACAGAA TACTATATGT 240 ACTGGGTGAA GCAGAGGCCT AAACAGGGCC TGGAATTAGT AGGAAGGATC GATCCTGAAG 300 ACGGTAGTAT TGATTATGTT GAGAAGTTCA AAAAGAAGGC CACACTGACT GCAGATACAT 360 CGTCCAACAC AGCCTACATG CAACTCAGCA GCCTGACATC TGAGGACACA GCAACCTATT 420 TTTGTGCTAG GGGAAAATTC AACTATCGAT TTGCTTACTG GGGCCAAGGC ACCCTCGTCA 480 CAGTCTCCTC A 491
- (2) INFORMATION FOR SEQ ID NO: 86:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 137 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: polypeptide
  - (ix) FEATURE:
- (A) NAME/KEY: Amino acid sequence of chimeric LO-CD2a  $V_{\scriptscriptstyle H}$  chain.
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86:

Met	Lys	Cys	Arg	Trp	Ile	Ile	Leu	Phe	Leu
-19				-15					-10
Met	Ala	Val	Ala	Thr	Gly	Val	Asn	Ser	Glu
				-5				-1	+1
Val	Gln	Leu	Gln	Gln	Ser	Gly	Pro	Glu	
			5					10	
Leu	Gln	Arg	Pro	Gly	Ala	Ser	Val	Lys	Leu
				15					20
Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Ile	Phe	Thr
				25					30
Glu	Tyr	Tyr	Met	Tyr	Trp	Val	Lys	Gln	Arg
				35					40
Pro	Lys	Gln	Gly	Leu	Glu	Leu	Val	Gly	Arg
				45					50
Ile	Asp	Pro	Glu	Asp	Gly	Ser	Ile	Asp	Tyr
				55					60
Val	Glu	Lys	Phe	Lys	Lys	Lys	Ala	Thr	Leu
				65					70
Thr	Ala	Asp	Thr	Ser	Ser	Asn	Thr	Ala	Tyr
				75					80
Met	Gln	Leu	Ser	Ser	Leu	Thr	Ser	Glu	Asp
				85					90
Thr	Ala	Thr	Tyr	Phe	Cys	Ala	Arg	Gly	Lys
				95					100
Phe	Asn	Tyr	Arg	Phe	Ala	Tyr	Trp	Gly	Gln
				105					110

Gly Thr Leu Val Thr Val Ser Ser 

(2)		I	NFOR	MATI	ON F	OR S	EQ I	D NO	: 87:			
		(	i)	SEQU	ENCE	СНА	RACT	ERIS	TICS:			
				(A)	LEN	GTH:	112	ami	no acids			
				(B)	TYP	E:	amin	o ac	id			
				(C)	STR	ANDE	DNES	S:				
				(D)	TOP	OLOG	Υ:	line	ar			
		(	ii)	MOLE	CULE	TYP	E:	poly	peptide			
		(	ix)	FEAT	URE:							
				(A)	NAM	E/KE	Υ:	Rat	LO-CD2a	light	chain	variable
					reg	ion.						
		(:	xi)	SEQUI	ENCE	DES	CRIP	TION	: SEQ II	NO: 8	7:	
Asp	Val	Val	Leu	Thr	Gln	Thr	Pro	Pro	Thr			
				5					10			
Leu	Leu	Ala	Thr	Ile	Gly	Gln	Ser	Val	Ser			
				15					20			
Ile	Ser	Cys	Arg	Ser	Ser	Gln	Ser	Leu	Leu			
				25					30			
His	Ser	Ser	Gly	Asn	Thr	Tyr	Leu	Asn	Trp			
				35					40			
Leu	Leu	Gln	Arg	Thr	Gly	Gln	Ser	Pro	Gln			
				45					50			
Pro	Leu	Ile	Tyr	Leu	Val	Ser	Lys	Leu	Glu			
				55					60			

Ser Gly Val Pro Asn Arg Phe Ser Gly Ser

65 70

Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile

75 80

Ser Gly Val Glu Ala Glu Asp Leu Gly Val

85 90

Tyr Tyr Cys Met Gln Phe Thr His Tyr Pro

95 100

Tyr Thr Phe Gly Ala Gly Thr Lys Leu Glu

105 110

Leu Lys

- (2) INFORMATION FOR SEQ ID NO: 88:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 112 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: polypeptide
  - (ix) FEATURE:
    - (A) NAME/KEY: Humanized LO-CD2a light chain variable region.
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

Asp Val Val Met Thr Gln Ser Pro Pro Ser

5 10

Leu Leu Val Thr Leu Gly Gln Pro Ala Ser

				15					20	
Ile	Ser	Cys	Arg	Ser	Ser	Gln	Ser	Leu	Leu	
				25					30	
His	Ser	Ser	Gly	Asn	Thr	Tyr	Leu	Asn	Trp	
				35					40	
Leu	Leu	Gln	Arg	Pro	Gly	Gln	Ser	Pro	Gln	
				45					50	
Pro	Leu	Ile	Tyr	Leu	Val	Ser	Lys	Leu	Glu	
				55					60	
Ser	Gly	Val	Pro	Asp	Arg	Phe	Ser	Gly	Ser	
				65					70	
Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Lys	Ile	
				75					80	
Ser	Gly	Val	Glu	Ala	Glu	Asp	Val	Gly	Val	
				85					90	
Tyr	Tyr	Cys	Met	Gln	Phe	Thr	His	Tyr	Pro	
				95					100	
Tyr	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Leu	Glu	
				105					110	
Ile	Lys									
(2)		IN	IFORM	IATIC	ON FO	OR SE	EQ II	NO:	89:	
		(i	.) S	SEQUE	ENCE	CHAF	RACTE	ERIST	CICS:	
			(	(A)	LENG	TH:	112	amin	o acid	s
			(	(B)	TYPE	: a	mino	aci	.d	

(C)

STRANDEDNESS:

		(:	ii)	MOLE	CULE	TYP	<b>E:</b> ]	poly	pep	tide	·		
		(:	ix)	FEAT	URE:								
				(A)	NAMI	E/KE	Υ:	Lig	ht	chain	vairable	region	of
				HUM5	400								
		(:	xi)	SEQU!	ENCE	DES	CRIP'	TION	:	SEQ ID	NO: 89:		
Asp	Val	Val	Met	Thr	Gln	Ser	Pro	Leu	Se	r			
				5					1	0			
Leu	Pro	Val	Thr	Leu	Gly	Gln	Pro	Ala	Se	r			
				15					2	0			
Ile	Ser	Cys	Arg	Ser	Ser	Gln	Ser	Leu	Va	1			
				25					3	0			
Tyr	Ser	Asp	Gly	Asn	Thr	His	Leu	Asn	Tr	p			
				35					4	0			
Phe	Gln	Gln	Arg	Pro	Gly	Gln	Ser	Pro	Arg	g			
				45					5	0			
Arg	Leu	Ile	Tyr	Lys	Val	Ser	Asn	Arg	Asj	p			
				55					6	0			
Ser	Gly	Val	Pro	Asp	Arg	Phe	Ser	Gly	Sei	r			
				65					70	0			
Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Lys	Ile	e			
				75					80	ס			
Ser	Arg	Val	Glu	Ala	Glu	Asp	Val	Gly	Va]	L			
				85					90	)			
Tyr	Tyr	Cys	Met	Gln	Gly	Thr	His	Trp	Pro	•			
				95					100	)			

(D) TOPOLOGY: linear

Tyr	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Leu	Glu
				105					110

Ile Lys

(2)	INFORMATI	ON FOR SEQ ID NO: 90:									
	(i) SEQU	(i) SEQUENCE CHARACTERISTICS:									
	(A)	LENGTH: 807 bases									
	(B)	TYPE: nucleic acid									
	(C)	STRANDEDNESS: single									
	(D)	TOPOLOGY: linear									
	(ii) MOLE	CULE TYPE: polynucleotide									
	(ix) FEAT	URE:									
	(A)	NAME/KEY: Nucleotide sequence	encoding								
	humanized	LO-CD2a light chain variable region.									
	(xi) SEQU	ENCE DESCRIPTION: SEQ ID NO: 90:									
AAGCTTCATG	ATGAGTCCTG TC	CAGTCCCT GTTTCTGTTA TTGCTTTGGA TTCTGGGTAA	60								
GTAGAGAATG	AGTTACAGGA CA	AGAATGGG GATGGAGGAT GAGTTCTGAC TGCCCATGTT	120								
GGCTGTCCAT	GTGTGGTAAG GC	AGGTCCTA TTTTCTAAGA TGGACACTTG AGATTCCATT	180								
ACTTGATAAT	GAGAAATTAC AG	ATGAGATA GGATTTGTGC TAAGAGGATT CTAATGTAGA	240								
TGAGAAGGTG	TATGCCATTT AG	GATCTGCA ACCGAATTGT TTTGTGAAAA AGCATTTGGT	300								
ATATTTTTA	AAAATCACAA AA	CACACCGG GATCTCACAG GAAATGAGTA ACAAAAAGTA	360								
ATTCACAAAG	ATTGGTTGCA AA	TTTTGCAC ATAACTTTGT TCTGATCTAT TATAATTTCA	420								
GGAACCAATG	GTGATGTTGT GA	IGACCCAG AGTCCACCTT CATTATTGGT AACCTTGGGA	480								
CAACCAGCTT	CCATCTCTTG CAG	GGTCAAGT CAGAGTCTCT TACATAGTAG TGGAAACACC	540								

600

660

TATTTAAATT GGTTGCTACA GAGGCCAGGC CAATCTCCAC AGCCGCTAAT TTATTTGGTA

TCCAAACTGG AATCTGGGGT CCCCGACAGG TTCAGTGGCT CAGGGAGTGG AACAGATTTC

ACACTCAAAA TCAGTGGAGT GGAAGCTGAG GATGTGGGGG TTTATTACTG CATGCAATTT	720							
ACCCATTATC CGTACACGTT TGGACAAGGG ACCAAGCTGG AAATCAAACG TGAGTAGAAT								
TTAAACTTTG CTTCCTCAGT TGGATCC								
(2) INFORMATION FOR SEQ ID NO: 91:								
(i) SEQUENCE CHARACTERISTICS:								
(A) LENGTH: 132 amino acids								
(B) TYPE: amino acid								
(C) STRANDEDNESS:								
(D) TOPOLOGY: linear								
(ii) MOLECULE TYPE: polypeptide								
(ix) FEATURE:								
(A) NAME/KEY: Humanized LO-CD2a light	chain							
variable region.								
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:								
Met Met Ser Pro Val Gln Ser Leu Phe Leu Leu								
-20 -15 -10								
Leu Leu Trp Ile Leu Gly Thr Asn Gly Asp								
-5 -1 +1								
Val Val Met Thr Gln Ser Pro Pro Ser								
5 10								
Leu Leu Val Thr Leu Gly Gln Pro Ala Ser								
15 20								
Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu								
25 30								
His Ser Ser Gly Asn Thr Tyr Leu Asn Trp								

Leu	Leu	Gln	Arg	Pro	Gly	Gln	Ser	Pro	Gln	
				45					50	
Pro	Leu	Ile	Tyr	Leu	Val	Ser	Lys	Leu	Glu	
				55					60	
Ser	Gly	Val	Pro	Asp	Arg	Phe	Ser	Gly	Ser	
				65					70	
Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Lys	Ile	
				75					80	
Ser	Gly	Val	Glu	Ala	Glu	Asp	Val	Gly	Val	
				85					90	
Tyr	Tyr	Cys	Met	Gln	Phe	Thr	His	Tyr	Pro	
				95					100	
Tyr	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Leu	Glu	
				105					110	
Ile	Lys									
(2)		IN	IFORI	ITA	ON FO	OR SE	EQ II	NO:	92:	
		( i	.) §	SEQUE	ENCE	CHAF	RACTI	ERIST	CICS:	
			(	(A)	LENG	TH:	118	amir	o acio	aƙ
			(	(B)	TYPE	E: a	umino	aci	.d	
			(	(C)	STRA	NDEL	NESS	3:		
			(	(D)	TOPO	LOGY	<b>:</b> 1	inea	ır	

35

40

(ii) MOLECULE TYPE: polypeptide

(ix) FEATURE:

(A) NAME/KEY: Rat LO-CD2a heavy chain variable region. (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92: Glu Val Gln Leu Gln Gln Ser Gly Pro Glu 5 10 Leu Gln Arg Pro Gly Ala Ser Val Lys Leu 15 20 Ser Cys Lys Ala Ser Gly Tyr Ile Phe Thr 25 30 Glu Tyr Tyr Met Tyr Trp Val Lys Gln Arg 35 40 Pro Lys Gln Gly Leu Glu Leu Val Gly Arg

45 50

Ile Asp Pro Glu Asp Gly Ser Ile Asp Tyr 55 60

Val Glu Lys Phe Lys Lys Lys Ala Thr Leu 65 70

Thr Ala Asp Thr Ser Ser Asn Thr Ala Tyr 75 80

Met Gln Leu Ser Ser Leu Thr Ser Glu Asp 85 90

Thr Ala Thr Tyr Phe Cys Ala Arg Gly Lys 95 100

Phe Asn Tyr Arg Phe Ala Tyr Trp Gly Gln 105 110

Gly Thr Leu Val Thr Val Ser Ser

(2)

INFORMATION FOR SEQ ID NO: 93:

		(i	) s	EQUE	NCE	CHAR	ACTE	RIST	'ICS:			
			(	A)	LENG	TH:	118	amin	o acids			
			(	В)	TYPE	: a	mino	aci	.d			
			(	(C)	STRA	NDED	NESS	<b>:</b>				
			(	(D)	TOPO	LOGY	: 1	inea	ır		0	
		(i	.i) M	OLEC	ULE	TYPE	: p	olyr	eptide			
		(i	.x) F	EATU	TRE:							
			(	(A)	NAME	E/KEY	<b>7:</b>	Hun	nanized	LO-CD2a	heavy	chain
			7	varia	ble	regi	on.					
		(х	ai) S	SEQUE	ENCE	DESC	RIPT	CION:	SEQ I	D NO: 93:		
Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu			•
				5					10			
Val	Lys	Lys	Pro	Gly	Ala	Ser	Val	Lys	Val			
				15					20			
Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr			
				25					30			
Glu	Tyr	Tyr	Met	Tyr	Trp	Val	Arg	Gln	Ala			
				35					40			
Pro	Gly	Gln	Gly	Leu	Glu	Leu	Met	Gly	Arg			
				45					50			
Ile	Asp	Pro	Glu	Asp	Gly	Ser	Ile	Asp	Tyr			
				55					60			
Val	Glu	Lys	Phe	Lys	Lys	Lys	Val	Thr	Leu			

65 70 Thr Ala Asp Thr Ser Ser Ser Thr Ala Tyr 75 80 Met Glu Leu Ser Ser Leu Thr Ser Asp Asp 85 90 Thr Ala Val Tyr Tyr Cys Ala Arg Gly Lys 95 Phe Asn Tyr Arg Phe Ala Tyr Trp Gly Gln 105 110 Gly Thr Leu Val Thr Val Ser Ser 115 (2) INFORMATION FOR SEQ ID NO: 94: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 123 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: (D) TOPOLOGY: linear (ii) MOLECULE TYPE: polypeptide (ix) FEATURE: (A) NAME/KEY: Human Amu 5-3 heavy chain variable region. (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94: Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val 15 20

Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr
				25					30
Gly	Tyr	Tyr	Met	His	Trp	Val	Arg	Gln	Ala
				35					40
Pro	Gly	Gln	Gly	Leu	Glu	Trp	Met	Gly	Arg
				45					50
Ile	Asn	Pro	Asn	Ser	Gly	Gly	Thr	Asn	Tyr
				55					60
Ala	Gln	Lys	Phe	Gln	Gly	Arg	Val	Thr	Met
	•			65					70
Thr	Arg	Asp	Thr	Ser	Ile	Ser	Thr	Ala	Tyr
				75					80
Met	Glu	Leu	Ser	Arg	Leu	Arg	Ser	Asp	Asp
				85					90
Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Arg	Gly	Arg
				95					100
Thr	Glu	Tyr	Ile	Val	Val	Ala	Glu	Gly	Phe
				105					110
Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr
				115					120
Val	Ser	Ser							

- (2) INFORMATION FOR SEQ ID NO: 95:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 701 bases
    - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: polynucleotide

## (ix) FEATURE:

•(1)

- (A) NAME/KEY: Nucleotide sequence encoding LO-CD2a heavy chain variable region.
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:

AAGCTTCATG	AAATGCAGGT	GGATCATCCT	CTTCTTGATG	GCAGTAGCTA	CAGGTAAGGC	60
ACTCCCAAGT	CCTAAACTTG	AGAGATCATA	CACTTGGGAG	ACAGTGACAC	TATCTTTGGA	120
TTTCTTTCAA	CAGGGGTCAA	CTCACAGGTG	CAGCTGGTGC	AGTCTGGGGC	TGAGGTGAAG	180
AAGCCTGGGG	CCTCAGTGAA	GGTCTCCTGC	AAGGCTTCTG	GATACACCTT	CACCGAGTAC	240
TATATGTACT	GGGTGCGACA	GGCCCCTGGA	CAAGGGCTTG	AGCTGATGGG	AAGGATCGAT	300
CCTGAAGACG	GTAGTATTGA	TTATGTTGAG	AAGTTTAAGA	AAAAGGTCAC	CCTGACCGCT	360
GACACGTCCT	CTAGCACAGC	CTACATGGAG	CTGAGCAGCC	TGACCTCTGA	CGACACGGCC	420
GTGTATTACT	GTGCGAGAGG	AAAGTTTAAC	TATAGGTTTG	CTTACTGGGG	CCAAGGAACC	480
CTGGTCACCG	TCTCCTCAGG	TGAGTCCTTA	CAACCTCTCT	CTTCTATTCA	GCTTAAATAG	540
ATTTTACTGC	ATTTGTTGGG	GGGGAAATGT	GTGTATCTGA	ATTTCAGGTC	ATGAAGGACT	600
AGGGACACCT	TGGGAGTCAG	AAAGGGTCAT	TGGGAGCCCG	GGCTGATGCA	GACAGACATC	660
CTCAGCTCCC	GGACTTCATG	GCCAGAGATT	TATAGGGATC	С		701

## (2) INFORMATION FOR SEQ ID NO: 96:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 137 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ix) FEATURE: Humanized LO-CD2a heavy chain (A) NAME/KEY: variable region. (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96: Met Lys Cys Arg Trp Ile Ile Leu Phe Leu -15 -10 -19 Met Ala Val Ala Thr Gly Val Asn Ser Gln -1 -5 Val Gln Leu Val Gln Ser Gly Ala Glu 10 5 Val Lys Lys Pro Gly Ala Ser Val Lys Val 20 15 Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr 30 25 Glu Tyr Tyr Met Tyr Trp Val Arg Gln Ala 35 Pro Gly Gln Gly Leu Glu Leu Met Gly Arg 45 50 Ile Asp Pro Glu Asp Gly Ser Ile Asp Tyr 60 55 Val Glu Lys Phe Lys Lys Lys Val Thr Leu 70 65 Thr Ala Asp Thr Ser Ser Ser Thr Ala Tyr

(ii) MOLECULE TYPE: polypeptide

75

Met Glu Leu Ser Ser Leu Thr Ser Asp Asp

85 90

Thr Ala Val Tyr Tyr Cys Ala Arg Gly Lys

95 100

Phe Asn Tyr Arg Phe Ala Tyr Trp Gly Gln

105 110

Gly Thr Leu Val Thr Val Ser Ser

115